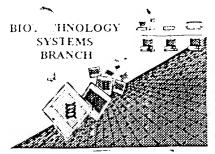
RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	10 1002,344	
Source:	0165	· <u>~</u>
Date Processed by STIC:	12/12/01	

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS. PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §\$1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2Kcompliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary.

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER:
ATTN: NEW RULES CASES	: PLEASE DISREGARD ENGLISH "ALPHA"	HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
Wrapped Nucleics Wrapped Aminos		apped" down to the next line. This may occur if your file ting it. Please adjust your right margin to .3; this will
2Invalid Line Length	The rules require that a line not exceed 72 c	haracters in length. This includes white spaces.
3 Misaligned Amino Numbering	The numbering under each 5th amino acid is use space characters, instead.	misaligned. Do not use tab codes between numbers,
4Non-ASCII	The submitted file was not saved in ASCII(I ensure your subsequent submission is sav	(XXX) text, as required by the Sequence Rules. Please ed in ASCII text.
5Variable Length	each n or Xaa can only represent a single	enting more than one residue. Per Sequence Rules, residue. Please present the maximum number of each in the <220>-<223> section that some may be missing
6PatentIn 2.0 "bug"	previously coded nucleic acid :equence Ple	the <220>-<223> section to be missing from amino acide in the would automatically generate this section from the case minually copy the relevant <220>-<223> section to applies to the mandatory <220>-<223> sections for
7Skipped Sequences (OLD RULES)	(2) INFORMATION FOR SEQ ID NO X: (i) SEQUENCE CHARACTERISTIC	sleave insert the following lines for each skipped sequence insert SEQ ID NO where "X" is shown) CS (Do not insert any subheadings under this heading) RO X (insert SEQ ID NO where "X" is shown)
	Please also adjust the "(u) NUMBER OF SE	QUENCES "response to include the skipped sequences
8Skipped Sequences (NEW RULES)	Sequence(s) mussing If intentional -:210> sequence id number <400> sequence id number (000	, please insert the following lines for each skipped sequence
9U∞ of n's or Xaa's (NEW RULES)		n the Sequence Listing. 223> is MANDATORY if n's or Xaa's are present cation of n or Xaa, and which residue n or Xaa represents
0Invalid <213> Response	Per 1.823 of Sequence Eules, the only valid scientific name (Genus/species) < 220> < 22 is Artificial Sequence	<2135 responses are: Unknown, Artificial Sequence, or 35 section is required when <2135 response is Unknown or
1Use of <220>	Use of <220> to <223> is MANDATORY if "Unknown." Flease explain source of genetic	Feature" and associated numeric identifiers and responses [<213> "Organism" response is "Artificial Sequence" or c material in <220> to <223> section (5. No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Eules)
	resulting in missing mandatory numeric iden	PatentIn version 2.0. This causes a corrupted file, tufiers and responses (as indicated on raw sequence or any other manual means to copy file to floppy disk

TATE: 12/12/2001

OIPE

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PATENI AFTITATI N. US/10/002,344
                                                               IIML: 14:28:54
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                     Output Set: N:\CRF3\12112001\I002344.raw
      3 <110 > APPLICANT: Recipon, Herve
             Sun, Yongming
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                                                                   The type of errors shown exist throughout
              Tiu, Chenghua
                                                                   the Sequence Listing Please check subsequent
              Chen, Sei-Yu
                                                                   sequences for similar errors
              Turner, Leah
      9 <120> TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific
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     649 tyaqacatat attictytca tityotytti (taaycaaaa acatyticat ytitoaiaiy 240
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    •54 qqaqtqaaaq catttaaaat attacctate tittetetit cesetaetga ttaaqqacti 540
    \mathfrak{v}55 gradetteta ittictatatt iciattaeta taetggatae eelitatatti aacafactia 600
    656 tittaaatata tattiittaa aagidtataa dattoatoig tatoittioi adidaaada 660
    657 aggaetttag caeacattta catetttaat accatattat tattactaag attracttct 720
    658 agettitgaa geatattage tittageteat attitaaeae tettigetti agiatteeae 786\,
    n59 firstiticing attitutiff circultacing adjacently the q fixed that each a 846
    600 gayttiqtga gitiqaaaaci taqoiticqiq talciqaaya iqrqittatt tigotoocac 906
    n61 tetigitatata aaccaetigia tigaaactigga ageteacagi tattitteta cageactitig 960
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RAW SEQUENCE LISTING

RAW SEQUENCE LISTING

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- DATE: LL/LL/LS-01 - DIME: 14:08:14

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output Sot: N:\CRF3\12112001\1002344.raw

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     672 qaqaqtiifa acthattiit aaantoteac cuqaftqiic fichtiifete aqqtataaat 1620
     \kappa^{*}3 teretraint griggerer engaging filteranger ettaggitt abiggerer 1680
     6\%4 tigitaitytt tiggggyddo aatttitaly atiacladaa aalytaayta coigtaldia 1\%40
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     676 transfriggt agetetyggt effections onlagginge consituting attititages 1369
     hTT caaaaqtatt tigugteeaa qtectatett qaqtqqttte etqeqetige tiqtqaetqe 1920
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     880 cayacaygat baltgeamma mmacetqqte ecamityeen mtatecatte mtagemeete 2100
     681 organizated godatoatag tygottitot, attactggod caaagagast titottiott 216)
     682 attittaaga atamotatgi attititaaa achittaaaa ataittaigo ataattioto 2220
     683 tgtttttgaa tgagaggaat aagattcagg agtattcact ctgccaccct 4acctagaag 2280
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     589 qaqqqtastt tebaciqbab baqaaaqaqb habtqhaqbb aqbaqaqtbb tqtaafaaqt 2540
     690 annuarritge artoetgeae elggaagaea gerathayet taytagaaag aatgetggae 270)
     591 tyqqaattoa gaaatyttot aqttoatitti ofaccactaa ytoatfyfac agottaggot 2769
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     694 araagragge Eqaqtectoe attetteage figeteajaa ataatetigee aggtaaaaga 294\%
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RAW SEQUENCE LISTING

1A11: 12/12/2

11ME: 14:38:04

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E--> 2526 ttcaqtcaca cacacantca cccactagca tcgctgtatc caatatcttc tctggatgtc 600
    252° aggadagete totoetogeog etcaaggace teaggoteta oftogaaggaa tojaagtotoe 600
     2528 tratattaaa aqaaaaqtaq caatqcaaaq caaaqaaqqc caaqtqcaaa tqtqcaqtqt 720
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E--> 2530 tqaaqacatq gaattggagg cagtgagaaa ggtggtcttt ncagagggag cagtgttgac 840
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    4351 ~2115 LENGIH: 47
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    4357
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    4359 Lys Asn Asn Trp Lys Lys Ile Ala Glu Ile Val Lou Lys Lou Thr Asn
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                  3 = 5
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RAW SEQUENCE LISTING

RAW SEQUENCE LISTING

FAIRNI AFFILMATI N: US/10/002,344 | ITME: 14:12*: ...

- HAIN: ll/ll/L l

light Ser : A:\Dex-2411.app

Tiph: Set: N:\CRF3\12112001\1002344.raw

Sectionally Armady Photoday Loss High Min Asp. Products Glad High Alad Had Asp.

E--> 5882 Met Glu Leu Glu Ala Val Arg Lys Val Val Phe Xaa Glu Gly Ala Val 5893 65

5885 leu für Ara Pro Leu

5886

5915 + 210 + SEO II NO: 246

 $5 \cdot 16 + 211 + 1 \cdot 10 \cdot 101 \cdot 11 \cdot 100 \cdot$

5917 - 242 - TYPE: PRI

5+18+213 - GRGANISM: Homo sapions

5920 + 400 + SEQUENCE: 246

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5925 20 2.5 31)

5927 Leu Arg Glin Gliu Gly Lys Tyr Phe Lys Arg Leu Cys Gliu Phe Val Ser

5928 40

5930 Val His Leu Phe Phe Val Giu Tyr Ile Leu Lêu Ile

Ę.,

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6203 + 400 + SEQUENCE: 261

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6205 11)

E--> 6207 Thr Phe Glu Ile Asn Glu Ser Xaa Leu Ser Gln Cys Val Ile Asp Asn 20 25

VERIFICATION SUMMARY

DAIF: 12/12/2 TIMB: Tight +

PATENT APPLIANT N: US/10/002,344

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L:65 M:341 W: 46: "n" or "Xaa" used, for SEQ ID#:2
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L:702 M:340 E (46) "n" or "Xaa" used: Feature required, for SEQ ID::25
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L:1044~\mathrm{M}:341~\mathrm{W} (46) "n" or "Xaa" used, for SEQ ID# 42
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L:1081 H:341 W (4n) "n" or "Xaa" used, for SEQ ID# 44
L:1143 M 341 W (45) "n" or "(aa" used, for SEQ ID# 47
L:1144 M 341 W _{\star} ,46) "n" or "Xaa" used, for SEQ ID# 4^{7}
1:1145~{
m M} 541 W (46) "n" or "Xaa" used, for SEQ ID# 47
I:1168 M 541 W: (46) "n" or "Kaa" used, for SEQ ID#548
Lill69 M 541 W_{\odot} [45] "h" or "Kaa" used, for SEQ ID# 48
               ..45) "n" or "Kaa" used; Feature required, for SEQ 10#:50
L:1218 M 540 E
1:12" H 441 W
                (4m) "n" or "Raa" used, for SEQ ID# 53
                460 "n" or "Xaa" ased, for SEQ ID# 55
L:1278 H :41 W
               - 460 "n" or "Maa" used, for SEQ ID#:53
1:1279 \text{ M} > 41 \text{ W}
L:1291 M :41 W
               46: "n" or "Kaa" used, for SEQ HD#.5:
L:1292 M 541 W 546; "n" or "Xaa" used, for SEQ 10# 57
L:1322 M 341 W [400 "n" or "Xaa" used, for SEQ ID# 55
L:1323 M 541 W 460 "n" or "Kaa" used, for SEQ ID#.55
               46: "n" or "Kaa" used, for SEQ ID#:55
L:1324 M >41 W
               460 "n" or "Kaa" used, for SEQ II# 55
L:1325 M 341 W
L:1326 M 341 W. .460 "n" or "Xaa" used, for SEQ ID# 55
                ,460 "n" or "Xaa" used: Feature required, for SEQ ID#:62
L:148! M +40 H
L:1757 M.341 W (46) "n" or "Naa" used, for SEQ ID#:70
L:1758 M 341 W (46) "n" or "Xaa" used, for SEQ ID# 79
L:1759 M 341 W - 400 "n" or "Xaa" used, for SEQ ID# 79
L:176@ M 341 W 460 "n" or "Xaa" used, for SEQ ID#.79
L:1821 M:341 W (46) "n" or "Aaa" used, for SEQ ID# 80
1.:1822~\mathrm{M} 341 W _{3}460 "n" or "Xaa" used, for SEQ ID# 80
L:1823 M:341 W (46) "n" or "Xaa" used, for SEQ ID#:80
               .,46) "n" or "Xaa" used, for SEQ ID# 80
L:1824 M 341 W
               (46) "n" or "Xaa" used, for SEQ ID# 83 (46) "n" or "Xaa" used, for SEQ ID# 83
L:1940 M:341 W
L:1941 M:341 W
                \pm 461 "n" or "Xaa" used, for SEQ ID#:83
L:1942 M:341 W
                     "n" or "Naa" used, for SEQ ID# 84
L:1963 M:341 W (46)
1:1979~\mathrm{M};341~\mathrm{W}-(46) "n" or "Maa" used, for SEQ III# 85
L:1980 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#.85
L:2123 M:341 W: (465 "n" or "Xaa" used, for SEQ ID#:90
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VERIFICATION SUMMARY

FATENT AFFECTATION: US/10,002,344

| LATE: |2/12/2001 |-|IMF: |4:28||*

Imput Set : A:\Dex-2411.app

n'; n' Set: N:\CRF3\12112001\1002344.raw

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1:2241 M:341 W: (48) "h" or "Xaa" Weed, for SEG ID#:500
1:2242 M:541 W: 465 "n" or "Xaa" used, for 3EQ ID#:96
1:2244 M:341 W: 46: "n" or "Naa" used, for 3EQ 1D#:96
1.12356 M:740 E: 460 "n" or "Xaa" used: Feature required, for SEQ He::100
1:2466 M::41 W: 46: "n" or "Xaa" used, for 3Eg ID::102
L:2467 M::41 W: 46: "n" or "Xaa" used, for 4FQ ID::102
1:2484 M: 41 W: .46; "n" or "Xaa" used, for 3EQ 1D#:103
1:2485 M::41 W: 46; "n" or "Xaa" used, for SEQ 1D#:10?
I:2526 M::46 E: 46: "n" or "Naa" used: Feature required, for SEQ ID= 105
M:340 Repeated in SeqNo 105
L:3789 M:258 W: Mandatory Feature missing. 4223 not found for SEQ ID= 159
1:3821 M:458 W: Mandatory Feature missing. <223 - not found for SEQ ID#:160
L:3917 M:258 W: Mandatory Feature missing, <227 not found for SEQ ID# 165
1:3920 M:\pm 58 W: Mandatory Feature missing, <225 hot found for SEQ ID#:105
1:3923 M:258 W: Mandatory Feature missing, \times 225 \times not found for SEQ ID# 105
L:4356 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#.184
L:4449 M:258 W: Mandatory Feature missing, 3223 not found for SEQ ID# 189
1.:4455 M:258 W: Mandatory Feature missing, ..23 not found for SEQ ID# 189
L:4516 M:258 W: Mandatory Feature missing, -225 not found for SEQ ID=.192
L:5123 M:25s W: Mandatory Feature missing, <22:+ not found for SEQ ID# 219
L:5126 M:258 W: Mandatory Feature missing, \ \ 22^{\circ} \ \  not found for SEQ ID# 219
1.5129 M:25% W. Mandatory Feature missing, \times 22\% not found for SEQ ID# 219
1.5132 M-25% W. Mandatory Feature missing, <225 - not found for SEQ 1D* 21%
1.5152 M 254 W. Mandatory Feature missing, \pm 22 \pm not found for SEQ ID# 220
1.05376 M 25\pi W. Mandatory Feature missing, \sqrt{2289} not found for SEQ ID# 224
1.(5613\ M\ 25\%\ W) Mandatory Feature missing, 3223\% not found for 3EQ ID#.236
L:5622 M 258 W. Mandatory Feature missing, \sim\!223 not found for SEQ ID# 236
1.:5625 M 25\% W Mandatory Foature m.ssing, <22\% not found for SEQ ID# 236
I::5829 M 254 W. Mandatory Feature missing, <2255 nct found for SEQ ID# 242
1.:5832 M 25% W. Mandatory Feature missing, <223% not found for SEQ ID#:242
L:5882 M 340 F \pm (46) "n" or "Xaa" used: Feature required, for SEQ ID# 2440
I:5902 M 25% W. Mandatory Feature missing, <223: not found for SEQ ID# 245
1:5905 M 258 W Mandatory Feature missing, <2230 not found for SEQ ID= 245
L:5924 M 349 E
                [46] "n" or "Xaa" used: Feature required, for SEQ ID#.246
\rm L:600^{\circ}\ M\ 258\ W Mandatory Feature missing, <223> not found for SEQ ID# 250
I:6010 M.258 W. Mandatory Feature missing, <223% not found for SEQ ID# 250
L:6207 M.340 E (46) "n" or "Xaa" used: Feature required, for SFQ ID= 261
1:6290 M 258 W Mandatory Feature missing, 223% not found for SEC ID#:264
L:6293 M:258 W. Mandatory Feature missing, <2237 not found for SEQ ID# 264
L:6296 M:2 8 W: Mandatory Feature missing, <223^\circ not found for SEQ ID# 264
1:6299~\mathrm{M}:258~\mathrm{W}: Mandatory Feature missing, \sim\!223^\circ not found for SEQ ID# 264
1.:6408 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID# 270
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